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Result
No.
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.Harimum Match 100%
Listr<sub>e</sub> 7 first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum Db, ~~q length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                     397
386.5
378.5
                                                                                                                                                                                                                                                                    Score
                                                                                          105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          October 11, 2002, 02:40:24; Search time 27 Seconds (without alignments) 922.640 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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: sp_archea:*
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49
19
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Copyright (c) 1993 - 2002 Compugen Ltd.
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sp_bacteria:*
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sp_rvirus:*
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sp_archeap:*
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sp_mammal:*
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sp_vertebrate:*
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Q9H7A0
Q93283
Q00833
Q9UVD9
Q95KK1
Q98BE8
                                               Q9EQ11
Q9UVC2
                                                                           Q96V43
Q9HFY8
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Q9DCZ3
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Q9d6i0 mus musculu
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Q9h7a0 homo sapien
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Q9h7a0 fumo sapien
Q9h7a0 fumo sapien
Q9543 aspergillus
Q9b43 aspergillus
Q9hfy8 colletotric
Q9eq11 mus musculu
Q9uvd9 alternaria
Q95kk1 macaca fasc
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 Q98be8 rhizobium
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78 10.2 223 2 045488 77 10.2 499 16 09ARK5 74.5 9.8 464 10 048967 73.5 9.6 589 16 09KEI1 73.5 9.6 589 16 09KEI1 73.5 9.4 183 2 093S62 72 9.4 185 2 093S62 71.5 9.4 485 2 093KE 70.5 9.2 180 16 09PAL1 70.5 9.2 202 4 09NVP2 70.5 9.2 688 2 09FBAL 70.5 9.2 688 2 09FBAL 70.5 9.2 688 2 09FBAL 70.5 9.2 180 16 09KN3 70.5 9.2 180 16 09KN3 70.5 9.2 688 2 09FBAL 70.5 9.2 688 2 09FBAL 70.5 9.2 180 10 004648 69.5 9.1 1609 10 004648 69.5 9.1 1609 10 004648 69.5 9.1 1609 10 004648 69.5 9.0 2506 471 17 09HMA9 68.5 9.0 1538 10 094HZ6 68 8.9 215 2 09JUF9 68 8.9 215 2 09JUF9 68 8.9 437 2 09JL249 68 8.9 1113 2 09JL249 68 8.9 1113 2 09JL249	
2 223 2 045488 2 464 10 048967 6 589 16 09KEI1 6 589 16 09KEI1 6 183 2 093662 4 485 2 09XAF0 0 4 550 5 019680 0 4 550 10 00YP2 1 202 4 09NVP2 2 202 4 09NVP2 2 202 4 09NVP2 2 180 10 026088 2 180 2 09FEBB 6 2 09FEBB 7 1 476 11 0042066 1 476 12 09XDN8 1 1609 10 004648 1 1609 10 004648 1 1763 2 09KX25 0 2506 12 09HMA9 0 1538 10 094XB6 0 1538 10 094XB6 0 1538 10 094XB6 0 1538 10 0910F9 9 467 5 0967XB 9 467 5 0967XB	
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Q45488 bacillus su Q938k5 caulobacter Q48967 zea mays (m Q9keil bacillus ha Q30772 pyrococcus Q9362 mycobacteri Q9xaf0 streptomyce Q19680 caenorhabdi Q9pal1 xylella fas Q9pv20 homo sapien Q96098 saccharomyce Q9fb28 streptomyce Q9fb28 streptomyce Q9fb28 streptomyce Q9fb28 streptomyce Q9nkn3 leishmania Q42066 equine herp Q9kdn8 bacillus ha Q440648 arabidopsis Q9k725 streptomyce Q9yd2 venezuelan Q9s213 streptomyce Q9hma9 halobacteri Q9wxb0 acidiphiliu Q94126 oryza sativ Q93096 candidatus Q910f9 pseudomonas Q911x2 streptomyce Q9f7x8 panulirus a Q35157 mus musculu Q91249 streptomyce	048967 09XE11 09XE11 093562 093562 099AF0 019680 09PAL1 09NVZ0 09NVZ0 09NKN3 042066 09KEN8 0
	048967 zea r 048967 zea r 098e11 bacil 030772 pyrocyc 03362 mycobb 09xaf0 strepi 019680 caenoi 09nvz0 homo r 09nvz0 homo r 09nvz0 homo r 09nvz0 homo r 09fb28 strepi 09fb28 strepi 09kdn8 bacil 09kdn8 bacil 09kd8 arab- 09kd8 arab- 00kd8 arab- 00kd8 arab- 00kd8 arab- 00kd8 arab- 00kd8

ALIGNMENTS

Q9D1F0 Q9D1F0 Q9D1F0 Q9D1F0 Q9D1F0 Q9D1F0 Q9D1F0 Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update) Q9D1F0 Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update) Q1-JUN-2005RIK ROTGEIN (RIKEN CDNA 1110012005 GENE). Q1110012005RIK POTEIN (RIKEN CDNA 111012005 GENE). Q1110012005RIK POTEIN (RIKEN CDNA 111012005 GENE). Q1110012005RIK POTEIN (RIKEN CDNA 111012005 GENE). Q110012005RIK POTEIN (RIKEN CDNA 111012005 GENE). Q1110012005RIK POTEIN (RIKEN CDNA 111 V. KORDINA H., Kasukawa T., Salto T., Okazaki T., Gojobori T., Bono H., Kasukawa T., Salto R. A Radota K., Jasaka K., Joshaka T., Salto R., Ashburner M., Batalov S., Casavant T., RA Salto T., Okazaki T., Gojobori T., Bono H., Kasukawa T., Salto R., Staubli R., Tomita M., Wagner L., Washio T., RA Salto T., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barshi G., RA Brownstein M.J., Bult C., Pletcher C., Fujita M., Gariboldi M., RA Brownstein M.J., Bult C., Pletcher C., Fujita M., Gariboldi M., RA Brownstein M.J., Bult C., Pletcher C., Fujita M., Gariboldi M., Lee N.H., RA Brownstein M.J., Bult C., Pletcher C., Fujita M., Gariboldi M., RA Brownstein M.J., Bult C., Pletcher C., Fujita M., Gariboldi M., RA Brownstein M., Bult C., Pletcher C., Fujita M., Gariboldi M., RA Brownstein M., Salto R., Kohenb
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RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

P. 'Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsud H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Saasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., ' wis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., ' wis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., ' wis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., ' wis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., ' wis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., ' wis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Sakai Y., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blab's J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blab's J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasenawa Y. Kawati u. Koheriki C.
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Best Local S
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                                                                                                                                                                                                              MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9DCZ3;
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AK003646; BAB22912.1; -. EMBL; BC003436; AAH03436.1; -. MGD; MGI:1913408; 1110012005Rik.
                                                                                                                                                                                                                                                                                           Wynshaw-Boris A., Yoshida
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                               Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                 Hayashizaki Y.;
                                                                                                                                                                                                                                                                Functional annotation of a full-length mouse
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62
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                                                                                                                                             Local Similarity
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                                                                                LRPAARRWR-NPIPEPETEDGDTDRLPEEIVQTCSYMFVDENTESNDALKVTELITRLTG 105
 RALQWVIPYIKIDSPLLNDYNGFLNEMKRVFGWEEDEDF
                                                               LRHNRRRRRVNPIPFPELFDGEMDKLPEFIVQTGSYMLVDDRTFDTDELKVTFLITRLKG
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Last sequence update)
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                             RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local :
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Q98SV9;
01-JUN-2001
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                 Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Actinopterygii: Neopterygii: Teleostei: Euteleostei: Neoteleostei:
                                                                                                                                                                        GAG-PROTEASE.
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
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SEQUENCE FROM N.A.
TRANSPOSON-SUSHI-SAN RETROTRANSPOSON;
MEDLINE-21321259; PubMed-11428463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21085660;
                                                                                    Acanthomorpha; Acanthopterygii; Percomorpha;
Tetraodontidae; Takifugu.
                                                                   NCBI_TaxID=31033;
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Pred. No. 2.1e
14; Mismatches
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Last annotation update)
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                                                                                                                                                                                                                                                              PRT;
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SEQUENCE
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SMART; SM00343; ZNF_CHC; I.
PROSITE; PS00141; ASP_PROTEASE; UNI
PROSITE; PS50175; ASP_PROT_RETROV;
PROSITE; PS50013; CHROMO_2; 1.
                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE-21218929; PubMed-11318613;
Ono R. Kobayashi S., Wagatsuma H.,
Kaneko-Ishino T., Ishino F.;
A Retrotransposon-Derived Gene, PEK
Located on Human Chromosome 7q21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Satoh S., Furukawa Y.; "Isolation of MEF3 like Submitted (SEP-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE=TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                      SEQUENCE
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43; Conserv
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Primates;
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                                                                                                      36965 MW;
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29.4%;
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the EMBL/GenBank/DDBJ

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    Last sequence update)
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Pred. No. 5.
   Score 137;
Pred. No. 5.
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5.5e-08;
hes 52;
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      DB 4;
.8e-07;
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Similarity

SEPPPE

PROTEIN)

sapiens (Human)

01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA: FLJ21125 FIS, CLONE CAS06077 (HYPOTHETICAL 32

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Q9H7A0

Q9H7A0; Q9H7A0; Q1-MAR-2001

PRELIMINARY;

PRT;

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ADD DE REPRESENTATION OF THE REPRESENTATION 
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Q9UPV1
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for large proteins in vitro.";
DNA Res. 6:197-205(1999).
EMBL; AB028974; BAA83003.1; -.
Interpro; IPR001878; Znf_CCHC.
Pfam; PF00098; zf-CCHC; 1.
SMART; SM00343; ZnF_C2HC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Homo sapiens (Human).
horvota; Metazoa; Chordata;
horvia; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kikuno R., Nagase T., Ishikawa K., Hirosawa M., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.
The complete sequences of 100 new cDNA clones from brain which co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UPV1;
01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                   LAPFMAQCQIFMEKSTRDFSVDRVRVCFVTSMMTGRAARWASAKLERSHYLMHNYPAFMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMKHVE
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                                                                                                                                                                                                                                    LPEFIVOTCSYMFVDENTFSNDALKVTFLITRLTGPALQWVIPYIRKESPLLNDYRGFLA 130
                                                                                                                                                                                                                                                                                                                                     RRRLSADPHATQRNSAEARGTMDGRVQLMKALLAGPLRPAARRWRNPIPFPETFDGDTDR 70
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                                                                                                                               EMKRVF 136
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                                                                                                                                                                                                                                                                                                                                                                                            37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 AA;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 137; DB 4;
Pred. No. 6.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DC14C265B92541EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 342;
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                                                                                                                                                                                                                                                                                                                                                                                              12;
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Best Local :
                              Matches
                                          Owery Match
Best Local S
                                                                                                     SEQUENCE FROM N.A.

TRANSPOSON-SUSHI-ICHI RETROTRANSPOSON;

POULTER R.T.M., Butler M.I.;

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ date EMBL; AP030881; AAC33525.1; ...

InterPro; IPR001878; Znf_CCHC.; I.

Pfam; PF00098; Zf-CCHC; 1.

PRINTS; PR00939; C2HCZNFINGER.

SMART; SM00343; Znf_CCHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        latches
                                                                                                                                                                                                                                                                                                                                                               Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               O93283 PRELIMINARY; PRT; 371-AA.
O93283;
O1-NOV-1998 (TrEMBLrel. 08, Created)
O1-NOV-1998 (TrEMBLrel. 08, Last sequence up
O1-DEC-2001 (TrEMBLrel. 19, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; Nakamura Y., Isogai T., Sugano S.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                           Poulter R., Butler M.;
Pa retrotransposon family from the
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TRANSPOSON-SUSHI-ICHI RETROTRANSPOSON;
MEDLINE=98382517; PubMed=9714821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; AK024778; BAB14998.1; .. EMBL; BC011679; AAH11679.1; -.
                                                                                    Polyprotein;
SEQUENCE 3
                                                                                                                                                                                                                                                      "A retrotransposon fami
Gene 215:241-249(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. SEQUENCE 303 AA; 3
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=31033;
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  2 RAPTLDMRFRRRLSADPHATQRNSAEARGT---
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                             l Similarity
.44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                371 AA;
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                                                                                                Zinc-finger
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Primates;
                                                                                   40540 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32478 MW;
                           16.0%; Sc
24.7%; Pr
tive 21;
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                             Score 122; DB Pred. No. 3.2e 21; Mismatches
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Pred. No. 7.8
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                                                                                   617926FC010730AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                 pufferfish (fugu) Fugu rubripes.";
                             DB 13;
3.2e-05;
les 67;
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.on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                   databases
                                                                                   CRC64;
                                                     Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                              Indels
----MDGR 35
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                              46;
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RESULT COOKS OF THE COOKS OF TH RESULT 10 Q96V43 S 밁 Qy 밁 밁 20 B δÃ В Query Match Best Local S Matches 29 Q96V43; Q96V43; Q1-DEC-2001 Pfam; PF00098; zf-CCHC; I.
PRINTS; PR00939; CZHCZNFINER.
SMART; SM00343; ZDF_CZHC; 1.
POlyprotein; Zinc-finger.
SEQUENCE 853 AA; 99422 MW; 000833 SEQUENCE FROM N.A.
STRAIN-NRRL 19997; TRANSPOSON-AFRTL-1;
MEDLINE-95314240; PubMed-7793909;
MCAlpin C.E., Mannarelli B.;
"Construction and characterization of Aspergillus flavus.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiom
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; 01-DEC-2001 01-DEC-2001 EMBL; L34658; AAA88790. InterPro; IPR001878; Zn oxysporum."; Mol. Gen. Genet. 249:637-647(1995). EMBL; L34658; AAA88790.1; STRAIN=F. SP. LYCOPERSICI 42-87; MEDLINE=96132549; PubMed=8544829; Anaya N., Roncero M.I.; "Skippy, a_retrotransposon from the Fusarium oxysporum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Hypocreales; mitosporic Hypocreales; Fusarium
NCBI_TaxID-5507; 01-NOV-1996 01-DEC-2001 POLYPROTEIN SEQUENCE FROM N.A. 01-NOV-1996 strains of Aspergillus NCBI_TaxID-5059; 100 131 160 102 9 47 08 36 14 72 RLTGPALQWVIPYIRKESPLLNDY 125 LASAANNGRDPGEVLKPSPPEYFDGTPSKLPTFLTQSRAFITYYPNQFRNDSAKVMYMAG 159 LRPAARRWRNPIPF----PETFDGDTDRLPEFIVQTCSYMFVDENTFSNDALKVTFLIT RTPTLPSPLERRYEA--HSAQLSSLQSELTKAFPTIQGETSELQSSSQTTSSTLSALSNQ ELLFRHQPSRFVSDEAKVGFITSLLADKALSWAIAAVDLDPRLSSDYSAFRREFKAVF 188 SYMEVDE-NTESNDALKVTELITRLTGPALQWVIPYIRKESPLLNDYRGELAEMKRVF 136 MSAMATVLASIIQKLGSDPGGAAPSEPSLPLSPRAEPNLASPRVFGGDFDLGKGFLHQ-C 130 RLIKTAAQWF-----QPIMNDY 176 Similarity (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLIEL 01, (TrEMBLIEL 01, (TrEMBLIEL 19, Conservative (FRAGMENT). PRELIMINARY; PRELIMINARY; 15.9%; Score 121; DB 3; 34.5%; Pred. No. 0.00012; Znf_CCHC. flavus."; . 12; Created)
Last sequence up Created) Last sequence update)
Last annotation update) PRT; 1AEDD18CFBBA5B06 CRC64; Mismatches 1252 fungal plant pathogen Fusarium 853 D DNA ₽ update) probe for update) Eurotiomycetes; Sordariomycetes; Length Indels distinguishing Aspergillus 12; Gaps 101

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Environ.

Microbiol. 61:1068-1072(1995).

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Best Local
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Best Local :
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Q1-MAR-2001
Q1-MAR-2001
Q1-DEC-2001
                                                                                                                                                                                                                        fungus Colletotrichum gloeosporioides
Curr. Genet. 0:0-0(2000).
EMBL; AF264028; AAG24791.1; -.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; I.
SMART; SM00343; Znf_CZHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fungus Aspergillus flavus.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF362957; AAL26311.1; ...
NON TER 1252 1252
                                                                                                                                                                                                                                                                                                                                                                                                   cingulata).
Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Okubara P.A., Tibbot B., McAlpin C.E., Hua S.-S.T.; "AfRTL-1, a retrotransposon-like element in the aflatoxin-producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appl.
                                                                                                                                                                                                                                                                                                     zhu P., Oudemans P.V.;
"A long terminal repeat retrotransposon Cgret from the phytopathogenic
                                                                                                                                                                                                                                                                                                                            TRANSPOSON-RETROTRANSPOSON CGRET;
                                                                                                                                                                                                                                                                                                                                                                              Glomerella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAG PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=5457;
                                                                                                                                                                                                                                                                                                                                                                                          Sordariomycetes
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                                                                                                                                                                                                     SEQUENCE
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                        135
                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A.
184
                                                126
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                                                                                                 66
                                                                                                                       25 SAEARGTMDGRVQLMKALL--AGPLRPAAR-----RWRNPIPFPETFDGDTDRLPEF 74
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                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIRNEQQDHIAQLDAQVGASAPKDAIGKVKLPKA---
ΙF
                                                LVQIRTYQAFHMGTFQNDTERVVHAATFLRGRALAWFEPL--QQEWLDNPVEKYSQEVRN 183
                        VF 136
                                                                        IVQTCSYMFVDENTFSNDALKVTFLITRLTGPALQWVIPYIRKESPLLNDYRGFLAEMKR 134
                                                                                                  NAAALKELQGRAREAQELKKEVATLRAAANVISAPVEGRERLKLNTPATFDGTPGQLKGH 125
185
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1 (TrEMBLrel. 16,
1 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                      Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                   97738 MW;
                                                                                                                                                               13.2%;
29.5%;
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25.4%;
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                                                                                                                                                               Score 101; DB 3;
Pred. No. 0.019;
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                                                                                                                                                                                                                                                                                         on cranberry.";
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                                                                                                                                                                          Length 837;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UVC2;
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                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SIMPSON M.L., Butler M., Poulter R.T.M.;
Simpson M.L., Butler M., Poulter R.T.M.;
"Functions of the integrase of retrotransposons: the integrase
"FT-1 element from Cladosporium fulvum.";
"FT-1 element from Cladosporium fulvum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GAG POLYPROTEIN (PUTATIVE GAG HOMOLOGUE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               evolve into new cellular functions Mol. Biol. Evol. 18:266-270(2001).
EMBL; AF302691; A6339979.1; -.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TremBLrel. 19, Last annotat MYELIN EXPRESSION FACTOR-3-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Dothideomycetes et Chaetothyriomycetes incertae My
Mycosphaerellaceae; mitosporic Mycosphaerellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
Seth D., Oliver R.P.;
"CfT-1, an LTR-retrotransposon in C
pathogen of tomato.";
Mol. Gen. Genet. 233:337-347(1992).
EMBL; AF051915; AAF21677.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cladosporium fulvum (Fulvia fulva).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00343; ZnF_C2HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Ty3/Gypsy retrotransposon fossils in mammalian genomes: did they evolve into new cellular functions?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21105984; PubMed=11158386;
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                                                                                                                                                               MEDLINE=92318885;
                                                                                                                                                                                               SEQUENCE FROM N.A. TRANSPOSON-CFT-1 I
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5499;
                                                                                                                                      McHale M.T., Roberts I.N., Noble S.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                  LTR-RETROTRANSPOSON;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26171 MW; DEA82A2E624F3974 CRC64;
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Pred. No.
                                                                                  in Cladosporium
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                                                                                                                                           Beaumont C.,
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ae; Cladosporium.
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                                                                                                                                                 Whitehead M.P.,
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                                                                                                                                                                                                                                                                                                                                              of the
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InterPro; IPR001878; EMBL; Z11866; CAA77890.1;

Znf_CCHC.

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RESULT 15
Q95KK1
ID Q95KK
AC Q95KK
DT Q1-DE
DT Q1-DE
DT Q1-DE
DT Q1-DE
DT Q1-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QUUVD

QUUVD

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GAG.

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AN (1)

RP SEQUE

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RC STRAI

RC STRAI

RC MEDLI

RA KANEKA

RT "REAL

RT ALTERI

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
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                     Q95KK1;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                             Q95KK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UVD9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00098; zf-CCHC; 1.
SMART; SM00343; ZnF_C2HC; 1.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternaria alternata.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alterna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00098; zf-CCHC; 1.
SMART; SM00343; ZnF_C2HC; 1.
  HYPOTHET ICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000886; ER_target.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR001878; Znf_CCHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Gen. Genet. 263:625-634
EMBL; AB025309; BAA89271.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alternaria alterna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaneko I., Tanaka A., Tsuge T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-15A; TRANSPOSON-LTR-RETROTRANSPOSON MEDLINE-20309324; PubMed-10852484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-5599
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01-MAY-2000
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                                                                                                                                                                                                                                   147
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                                                                                                                                                                                                                                                                                 8
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                                                                                                                                                                                                                                                                            TDRLPEFIVOTCSYMFVDENTFSNDALKVTFLITRLTGPALQWVIPYI 115
                                                                                                                                                                                                                                                                                                                             MRLLSPMASRLEALERSQAEGRSESSLGANTTPPLSTPVAEPAVR--KNKFPDPERFDGT 146
                                                                                                                                                                                                                                                                                                                                                                         MRFRRRLSADPHATQRNSAEARGTMDGRVQLMKALLAGPLRPAARRWRNPIPFPETFDGD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEFFYGDRVKFDTWVSQMDMYFLFNSMT---ENLKPIFATTFLRGRAQHWVKPFLRKYLD 75
                                                                                                                                                                                                                                   RGNYPGWKFECEGKLEYDCAMFPTEDARVRYVLSRTKDKANQVLLPWV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                     (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 19,
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39 AA; 73649 MW;
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  KDA PROTEIN.
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24.1%;
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Last sequence update)
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Pred. No. 0.83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from the plant pathogenic fungus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F792231FC75CC8CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4D3BA4B19AE0753A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                       61;
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                                                                                                                         Matches
                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                         Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca,
NCBI_TaxID=9541;
                                                                                                                      Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AB060816; BAB46835.1; -. Hypothetical protein.
SEQUENCE 400 AA; 46612 MW; 911D7B5ADD0EEB56 CRC64;
                                                                                                                                                                                                Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Suzuki Y., Sugano S., Hashimoto K.; "Isolation of full-length cDNA clones from macaque brain cDNA".
                                                                                                                                                                                                                                                TISSUE=CEREBELLUM CORTEX;
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                      libraries."
 11
                   86 ENTFSNDALKVTFLITRLTGPALQWVIPYIRKESPLLNDYRGFLAEMKRVF 136
EDHFPGGAERVAFLISFFTGEAKDWAISVTQEGSPLHANFPRFLDEIRKEF 61
                                                              19;
                                                              Conservative
                                                                         10.9%;
                                                            10;
                                                                           Score 83;
Pred. No.
                                                              Mismatches
                                                                           DB 6;
0.77;
                                                              22;
                                                                                         Length 400
                                                              Indels
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                                                                                                                                                                                                                                 Terao K.,
                                                            Gaps
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Search completed: October 11, Job time : 30 secs 2002, 02:43:08

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Result
No.
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Maximum DB
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    549.5
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Match
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Gapop 10.0 , Gapext 0.
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763
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l: /SIDS1/gcgdata/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT: *
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Listing first 45 summaries
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126
146
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AAB60475
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AAY25512
AAY26051
AAB60492
                                             AAG02068
AAY26054
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                                                                                          Human secreted pro
Human mature alpha
Human alpha helica
Human cell cycle a
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8307 Arabidopsis	AAG58307	21	272	•	69	
2066 Human	AAB3	21	77		69	
2065 Human	AAB32065	21	77		69	
2156 C glutamicum	AAG92156	22	363		70	
1 Cc	AAB8005	22	358	9.2	70	
9919 Corynebacterium	AAB79919	22	358		70	
4328 Novel	ABG04328	22	2386	•	70.5	
7559 Protein encoded	AAB07559	21	889	•	٠	
5627 Human	AAG7	22	245	9.2	•	
3610 Human	AAB4	21	243	9.2		
2988 Human	AAB92	22	202	9.2	70.5	
2808 Human	AAB92808	22	202	9.2	70.5	
	ABB50194	22	202	9.2	70.5	
1310 C glutamicum	AAG91310	22	397	9.4	71.5	
4688 Human	AAY94688	21	41	10.0	76	
5498 · Novel	ABG15498	22	676	10.0	76.5	
6052 Human	AAY26052	20	45	11.1	85	
4692 Human	AAY94692	21	43	17.2	131	
4694 Human	AAY94694	21	76	17.6	134	
4693 Human	AAY94693	21	57	17.6	134	
2148 Human	AAB42148	21	342	18.0	137	
5099 Novel	ABG15099	22	1607	18.3	139.5	
4689 Human	AAY94689	21	65	20.2	154	
4691 Human	AAY94691	21	98		157	
4690 Human	AAY94690	21	79		157	
6055 Human	AAY26055	20	44	21.5	164	
6057 Human	AAY26057	20	51		182	
6053 Human	AAY26053	20	74	24.0	183	
4674 Human	AAY94674	21	168	25.4	194	
4673 Human	AAY94673	21	184		197	
	AAY26058	20	65	26.3	201	
Novel	ABG12204	22	42	29.8	227	
2067 Human secreted	AAG0206	21	67	37.4	285	

ALIGNMENTS

RESULT 1 AAY59927 XXX PT XXX PT XXX PT XXX PR X P X P X X P X ₹XXB Myometrium; tumour; human; expressed sequence tag; EST; uterine myoma; treatment; carcinoma; cancer; gene therapy. AAY59927; AAY59927 standard; Protein; 144 Rosenthal A, 28-OCT-1999. Homo sapiens. Human myometrium tumour EST encoded protein 7. 28-JAN-2000 (first entry) (META-) METAGEN GES GENOMFORSCHUNG MBH. 17-APR-1998; DE19817947-A1 17-APR-1998; Specht T, 98DE-1017947. 98DE-1017947. Hinzmann B, Schmitt A, æ Pilarsky ú Dahl

New nucleic acid sequences expressed in uterine myoma, and derived polypeptides, for treatment of uterine carcinoma and identification therapeutic agents

and identification of

WPI; 1999-602380/52. N-PSDB; AAZ41965.

Claim

23;

Page

68;

86pp;

German

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Matches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel polypeptide sequences (I), fragments of (I) fragments and their encoding nucleic acids (II) which are highly expressed in human uterine myoma. (II) are used for recombinant expression of (I) and to isolate complete genes. (I) are used to identify agents suitable for treatment of uterine carcinoma, to directly treat this form of cancer (including expression from gene therapy vectors) and are used in a preparation for cancer treatment. (I) is also used for the generation of specific antibodies. (II) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed and therefore reduces the number of failures associated with the fact that ESTs from different
                                                                        21-JUL-1999;
08-SEP-1999;
10-NOV-1999;
                                                                                                                                                                                                                                                                                                  Cell cycle and proliferation protein: CCYPR; human; antagonist; gene therapy; detection; gene therapy; transgenic animal disease model; immune disorder; developmental disorder; cell signalling disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB60475 standard; Protein; 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myometrium tumour cDNA library derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue AAY59921-Y59940 represent protein fragments encoded by the human
                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                              Human cell cycle and proliferation protein CCYPR-23,
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB60475;
 Hillman JL,
Azimzai Y,
                                                                                                                                                                  01-FEB-2001
                                                                                                                                                                                               WO200107471-A2
                                                                                                                                                                                                                                                           menstrual
                                                                                                                                                                                                                                                                      cell proliferative disorder; cancer arteriosclerosis; asthma; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                              24-APR-2001
                                                                                                                                    21-JUL-2000;
                                          (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LLNDYRGFLAEMKRVFGWEEDEDF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ARAPTLDMRFRRRLSADPHATQRNSAEARGTMDGRVQLMKALLAGPLRPAARRWRNPIPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PETFDGDTDRLPEFIVQTCSYMFVDENTFSNDALKYTFLITRLTGPALQWVIPYIRKESP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARAPTLDMRFRRRLSADPHATQRNSAEARGTMDGRVQLMKALLAGPLRPAARRWRNPIPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PETFDGDTDRLPEFIVQTCSYMFVDENTFSNDALKVTFLITRLTGPALQWVIPYIRKESP
                                                                                                                                                                                                                                                         cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 AA;
Lal P,
Yang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                    2000WO-US19948
                                                                        99US-0145075.
99US-0153129.
99US-0164647.
                                                                                                                                                                                                                                                           disorder; bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
 Tang YT,
Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                           cancer; tumour; anaemia;
lergy; diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 763; DB 2v,
Pred. No. 1.3e-83;
Yue H, A
Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          æ
                                                                                                                                                                                                                                                            intection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST fragments represented
              Au-Young J,
 Patterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
 Bandman O;
C, Shah P
                                                                                                                                                                                                                                                                                                                                                agonist;
                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:23
                                                                                                                                                                                                                                                                                       epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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QΥ 밁 Ş

32 -

MDGRVQLIKALLALPIRPATRWARNPIPFPETFDGDTDRLPEFIVQTGSYMFVDENTFSS MDGRVQLMKALLAGPLRPAARRWRNPIPFPETFDGDTDRLPEFIVQTCSYMFVDENTFSN 91 Matches 106; Query Match Best Local

Similarity

74.2%;

Score 566; DB 22; Pred. No. 4.5e-60; """ u'ematches 3;

Length 113; Indels

0

Gaps

0

60

Conservative

4.

Sequence

113 AA;

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CC Sequences AAB60453-AAB60506 represent 54 human cell cycle and coliferation proteins (CCYPR), which are encoded by AAF5990-AAF59643. CC CYPR and agonists of CCYPR are used to treat diseases or conditions colored with decreased expression of functional CCYPR, while CCYPR CC antagonists are used to treat diseases or conditions associated with coverexpression of functional CCYPR. Monoclonal or polyclonal antibodies coverexpression be used in enzyme-linked immunosorbent assays (ELISA) or cc cradioimmunoasays to detect CCYPR. CCYPR itself may be used to detect cc compounds e.g., antibodies, oligonucleotides and proteins (receptors) cc that specifically bind to CCYPR, and in drug screening methods to ct identify compounds that modulate the activity of CCYPR. CCYPR correctly compounds that modulate the activity of CCYPR. CCYPR correctly can be used to generate transgenic animal models of human cc disease, and can be used in gene therapy in target cells with genetic can be compounded to the expression of CCYPR for the creatment or prevention of a disorder associated with CCYPR. CC Diseases which can be diagnosed, treated and prevented using CCYPR correctins, nucleic acids, agonists or antagonists include immune, concers including cancer. Specific examples of these disorders allergies, cliphetes mellities disorders of the menstrual cycle and infertions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cell cycle and proliferation proteins and polynucleotides are used to treat, diagnose and prevent immune, developmental and cell signaling disorders and cell proliferative disorders including cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAF59612
                                                                         diabetes mellitus,
                                               caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-112727/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 131;
                                                  bacteria.
                                                                         disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                         of the menstrual cycle and infections
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RESULT 3
ABG12205
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                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                31-MAR-2000;
23-AUG-2000;
                                        30-MAR-2001; 2001WO-US08631.
                                                                          WO200175067-A2
                                                                                          Homo sapiens
                                                                                                                                    Novel human diagnostic protein #12196.
                                                                                                                                                     18-FEB-2002
                                                                                                                                                                      ABG12205
                                                                                                                                                                                      ABG12205 standard; Protein; 142
                                                          11-OCT-2001
                                                                                                                                                                                                                                2000US-0540217
2000US-0649167
                                                                                                                                                     (first entry)
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(HYSE-) HYSEQ INC

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RESULT 4
AAG04029
ID AAG6
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AC AAG0
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OF OF COLOR
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DE Huma
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DE Huma
XX
Huma
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PON EP10
PN 06-5-5
PD 06-5-5
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID No 42564; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-639362/73.
N-PSDB; AAS76392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT,
                                                                                                                                                              Human secreted
                                                                                                                                                                                              06-OCT-2000
                                                                                                                                                                                                                              AAG04029;
                                                                                                                                                                                                                                                            AAG04029 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                             gene therapy;
                                                EP1033401-A2
                                                                                                                              Human; 5' EST;
                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                        60
                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 AA;
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                                                                                                                                                                                            (first entry)
                                                                                                                chromosome mapping.
                                                                                                                            expressed sequence tag; secreted protein; cDNA isolation
                                                                                                                                                            protein, SEQ ID NO: 8110
                                                                                                                                                                                                                                                          Protein; 106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 549.5; DB 22
Pred. No. 5.8e-58;
2; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 142;
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Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic by as a constant of the companies and the sequences. They are used to obtain upstream regularity companies and to decrease the constant partners.
                                                                                                                                                                                              Human alpha helical protein-1; Zalphal; helical cytokine; skin tone; growth hormone; erythropoletin; leptin; interleukin-10; gene therapy; chromosome xq27.3; FMR1; Fragile-X syndrome; cosmetic improvement; hypothalamic pituitary gonadal axis dysfunction; cardiovascular system; abnormal proliferative disorder; cancer; connective tissue dysfunction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; SEQ ID 8110; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                 AAY25512 standard; Protein; 126
                                                                                                                                                                                                                                                                                                                                  28-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                AAY25512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                  Homo sapiens
                                                                                                                                                                                 epidermal system; elasticity
                                                                                                                                                                                                                                                                                                Human mature alpha helical protein-1 Zalphal.
                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 MDGRVQLMKALLAGPLRPAARRWRNPIPFPETFDGDTDRLPEFIVQTCSYMFVDENTFSN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                    Location/Qualifiers
1..127
                                                                    /note= "mature protein fragment,
                                                                                     /label= Zalphal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.9%;
89.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 350; DB 21;
Pred. No. 3.8e-34;
3; Mismatches 5;
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                                                                    no start codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 106;
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17-JUN-1999

W09929720-A2

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AAY26051
ID AAY
XX AAY
XX AAY
XX AAY
XX BHUM
XX HUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents the mature protein fragment of a novel alpha helical protein-1 designated Zalphal from human pituitary gland cDNA library. Zalphal is predicted to be a four-helical protein similar to the family of helical cytokines represented by growth hormone, erythropoietin, leptin and interleukin-10. Zalphal gene was mapped to chromosome Xq27.3, in close proximity to FNRI, a gene linked to Fragile-X syndrome. Its transcription levels were found to be reduced or absent in Fragile-X patients. Zalphal transcripts were found at high levels in pituitary and aorta, and lower levels in brain, kidney, pancreas, prostrate, etc. Zalphal is supposed to be responsible for the hypothalamic-pituitary-gonadal axis dysfunction and connective tissue dysfunctions in Fragile-X patients. The Zalphal DNA is used in gene therapy for treating patients having a mutated Zalphal gene or lacking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy for treating patients having a mutated Zalphal gene or lacking the gene. Probes derived from Zalphal gene can be used to check abnormalities on X chromosome. Zalphal protein may be useful in the treatment of Fragile-X syndrome and abnormal proliferative disorders e.g. cancer. It can also be used for the growth, differentiation, maintenance and survival of connective tissues, particularly cardiovascular and epidermal systems and in imparting cosmetic improvements to normal
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                                                                                                                                                                          Human alpha helical precursor protein-1; Zalpha1; helical cytokine; growth hormone; erythropoletin; leptin; chromosome Xq27.3; FMX1; Fraglle-X syndrome; interleukin-10; connective tissue dysfunction; abnormal proliferative disorder; cancer; epidermal system; skin tone; hypothalamic pituitary gonadal axis dysfunction; cardiovascular system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalian alpha helical protein-1, designated Zalphal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-DEC-1997;
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Peptide
                                                                                             Homo sapiens.
                                                                                                                                                      cosmetic
                                                                                                                                                                                                                                                                                                                                                                    Human alpha helical precursor protein-1, 2alphal
                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY26051;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               connective tissues such as enhancement of skin tone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 ITRLTGPALQWVIPYIRKESPLLNDYRGFLAEMKRVFGWEEDED 143
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73 ISLLTGEAEEWVVPYIEMDSPILGDYRAFLDEMKQCFGWDDDED 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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   Location/Qualifiers 1..20
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Pred. No. 3e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ن
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                                                                                                                                                                                   cardiovascular system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 126;
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24-APR-2001

(first entry)

Human cell cycle and proliferation protein CCYPR-40, SEQ ID NO:40

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                                                                                                                                                                   RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as enhancement of skin tone and elasticity.
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                                                                                                                                                                                                                                                    ITRLTGPALQWVIPYIRKESPLLNDYRGFLAEMKRVFGWEEDED 143
                                                                                                                                                                                                                                                                                                             ISLLTGEAEEWVVPYIEMDSPILGDYRAFLDEMKQCFGWDDDED
                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
62; Conserv
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                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 AA;
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23..37
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21..146
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                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                        43.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                Score 335; DB 20;
Pred. No. 3.6e-32;
7; Mismatches 21
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Best Local :
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08-SEP-1999;
10-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to CCYPR may be used in enzyme-linked immunosorbent assays (ELISA) or radioimmunoasays to detect CCYPR. CCYPR itself may be used to detect compounds e.g., antibodies, oligonucleotides and proteins (receptors) that specifically bind to CCYPR, and in drug screening methods to identify compounds that modulate the activity of CCYPR. CCYPR nucleotides can be used to generate transgenic animal models of human disease, and can be used in gene therapy in target cells with genetic abnormalities with respect to the expression of CCYPR for the treatment or prevention of a disorder associated with CCYPR. Diseases which can be diagnosed, treated and prevented using CCYPR because the contract of the contrac
                                                                                                                                                                                                                                                                                                                                                                                             proteins, nucleic acids, agonists or antagonists include immune, developmental and cell signalling disorders, and cell proliferative disorders including cancer. Specific examples of these disorders include anaemia, epilepsy, arteriosclerosis, asthma, cancer, allergies, diabetes mellitus, disorders of the menstrual cycle and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proliferation proteins (CCYPR), which are encoded by AAF59590-AAF59643 CCYPR and agonists of CCYPR are used to treat diseases or conditions associated with decreased expression of functional CCYPR, while CCYPR antagonists are used to treat diseases or conditions associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cell cycle and proliferation proteins and polynucleotides are used to treat, diagnose and prevent immune, developmental and cell signaling disorders and cell proliferative disorders including cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell proliferative disorder; cancer; tumour; anaemia; arteriosclerosis; asthma; allergy; diabetes mellitus; menstrual cycle disorder; bacterial infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               overexpression of functional CCYPR. Monoclonal or polyclonal antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences AAB60453-AAB60506 represent 54 human cell cycle and proliferation proteins (CCYPR), which are encoded by AAF59590-AAF59643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 150; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-112727/12
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Azimzai Y,
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KALLAGPLRPAARRWRNPIPFPETFDGDTDRLPEFIVQTCSYMFVDENTFSNDALKVTFL 99
                                                                                                       RASLLRQVRPPS----CPVPFPETFNGESSRLPEFIVQTASYMLVNENRFCNDAMKVAFL 92
                                                                                                                                                                                                              62;
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                                                                                                                                                                                                                                                                                                                      146 AA;
                                                                                                                                                                                                              Conservative
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99US-0153129.
99US-0164647.
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Lu DAM,
                                                                                                                                                                                                                                       43.9%;
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                                                                                                                                                                                                                                    Score 335; DB 22;
Pred. No. 3.6e-32;
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Baughn MR,
                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patterson
                                                                                                                                                                                                                 21;
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     136
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n C, Shah
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RESULT 8
AAG02068
                                                                                 RESULT 9
AAY26054
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XXXXXX
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                         The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed CDNA libraries. Such ESTs are not well suited for isolating CDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic bunks. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG02068 standard; Protein; 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein, SEQ ID NO: 6149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; SEQ ID 6149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-2000; 2000EP-0200610
                                                                     AAY26054 standard;
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                             regulatory sequences
                                          AAY26054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
                                                                                                                                           61
                                                                                                                                                                                                                  32 MDGRVQLMKALLAGPLRPAARRWRNPIPFPETFDGDTDRLPEFIVQTCSYMFVDENTFSN 91
                                                                                                                                                                      92 DALKVT 97
                                                                                                                                                                                                 1 MXGRVQLMKALLAXPLRPAARRWRNPIPFPETFDGDTDRLPEFIVQTSSYMFVDENTFSN 60
                                                                                                                                             DALKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5' EST;
                                                                                                                                                                                                                                                            63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC02074.
                                                                                                                                                                                                                                                                                                                     66 AA;
                                                                                                                                           66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 forensic,
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0122487
                                                                   Protein; 110
                                                                                                                                                                                                                                                                         43.0%;
95.5%;
                                                                                                                                                                                                                                                                                                                                                and to design expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71pp + CD-ROM; English.
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                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                           Score 328; DB 21;
Pred. No. 9.2e-32;
                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Giordano
                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                 secretion
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                             Gaps
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28-SEP-1999

(first entry)

Human

Zalpha1

epitope-bearing protein fragment

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SOX CCCCCCCCCX PSX P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is an epitope-bearing protein derived from human alpha helical protein-1, Zalphal. The protein comprises helices A, B, C and D of mature Zalphal. It is used to raise specific antibodies which can be used for detection and purification of Zalphal. The Zalphal protein may be useful in the treatment of Fragile-X syndrome and abnormal proliferative disorders e.g. cancer. It can also be used for the growth, differentiation, maintenance and survival of connective tissues, particularly cardiovascular and epidermal systems and in imparting cosmetic improvements to normal connective tissues sur as enhancement of skin tone and elasticity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha helical protein-1; Fragile-X syndrome; cardiovascular system; connective tissue; abnormal proliferative disorder; cancer; skin tone; epidermal system; cosmetic improvement; skin tone; elasticity; Zalphal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09929720-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalian alpha helical protein-1, designated Zalphal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-385572/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                      18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                           ABG12203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG12203 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                           WO200175067-A2
                                                                                                                                                                                                                    food
                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #12194.
                                                                                                                                                                                                                                             Human; chromosome
                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 KALLAGPLRPAARRWRNPIPFPETFDGDTDRLPEFIVQTCSYMFVDENTFSNDALKVTFL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITRLTGPALQWVIPYIRKESPLLNDYRGFLAEMKRVFGWE 139
                                                                                                                                                                                                                 supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 70; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110
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                                                                                                                                                                                                                      medical
                                                                                                                                                                                                                 mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.4%; 59.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 316; DB 20;
Pred. No. 4.9e-30;
16; Mismatches 21
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30-MAR-2001; 2001WO-US08631.

W09929720-A2

Homo sapiens

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AAY26056
ID AAY2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC for identifying expressed genes. (I) is useful in gene therapy techniques control to restore normal activity of (II) or treat disease states involving control to treat disease states involving control to treat disease states involving control to treat disease states involving a polypeptide in tissue, as molecular weight markers and as conditional control to the state of the sequences of the sequences of the polypeptide and polynucleotide sequences have applications in conditionable for generic disorders or other traits to assess blodiversity amino acid sequences of data and products dependent on DNA and control to produce other types of data and products dependent on DNA and control to the sequence of the invention.

CC diagnostic amino acid sequences of the invention.
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PN XXX
                                                                                                                                                                                                                                                                     RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromo and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID No 42562; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biodiversity
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                                                                                       Alpha helical protein-1; Fragile-X syndrome; cardiovascular system; connective tissue; abnormal proliferative disorder; cancer; skin to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                      Human Zalphal epitope-bearing protein fragment 5.
                                                                                                                                                                         28-SEP-1999
                                                                                                                                                                                                       AAY26056;
                                                                                                                                                                                                                                       AAY26056 standard; Protein;
                                                            epitope.
                                                                         epidermal system;
                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                   88
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                                                                                                                                                                                                                                                                                                                                                   TFSNDALKVTFLITRLTGPALQWVIPYI -- RKESPLLNDYRGFLAEMKRVFGWEEDED 143
                                                                                                                                                                                                                                                                                                                                                                                   RG-TMDGRVQLMKALLAGPLRPAARRWRNPIPFPETFDGDTDRLPEFIVQTCSYMFVDEN 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                  69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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2000US-0649167.
                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 310.5; DB 22
Pred. No. 2.7e-29;
0; Mismatches 22;
                                                                             skin
                                                                              tone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 129;
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                                                                                                                                                                                                                                                                                                                         105
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10-DEC-1998;

10-DEC-1997;

97US-0987926 98WO-US26273. 17-JUN-1999

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RESULT 12
AAG02067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       connective tissues, particularly cardiovascular and epidermal systems and in imparting cosmetic improvements to normal connective tissues so as enhancement of skin tone and elasticity.
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                          N-PSDB; AAC02073
                                                                                                           Dumas Milne Edwards J,
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61 PILGDYRAFLDEMKQCFGWD 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein,
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                                                                                                           Duclert
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Claim 20;

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RESULT 13
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                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                       N-PSDB;
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                                                                                                                                                                                                                                                                                                                               Liu C,
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medical imaging; diagnostic; genetic disorder.
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Pred. No. 1.4e-26;
4; Mismatches 4
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                              The present sequence is an epitope-bearing protein derived from human alpha helical protein-1, Zalphal. It is used to raise specific antibodies which can be used for detection and purification of Zalphal. The Zalphal protein may be useful in the treatment of Fragile-X
                                                                                                                                                                                                  Claim 10; Pages 72-73; 73pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Zalphal epitope-bearing protein fragment 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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syndrome and abnormal proliferative disorders e.g. cancer. It can also be
                                                                                                                                                                                                                                                               Mammalian alpha helical protein-1, designated Zalphal
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 LTGPALQWVIPYIRKESPLLNDYRGFLAEMKRVFGWEEDEDF 144
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Pred. No. 7.1e-20;
1; Mismatches 0
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elasticity; Zalphal;
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WPI; 2000-572091/53

Presnell

SR

(ZYMO) ZYMOGENETICS

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RESULT 15
AAY94673
ID AAY94673
AC AAY94
XX O1-DE
DT 01-DE
XW Alpha
KW proll
KW degen
XX Homo
XX Homo
XX Homo
FT Pepti
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha-helical protein; zsig83; cell growth; differentiation; cancer; proliferation; chromosome 22q13.1-q13.2; cytostatic; vulneray; degenerative condition; metastasis; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used for the growth, differentiation, maintenance and survival of connective tissues, particularly cardiovascular and epidermal sys
                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                        Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human zsig83 protein sequence
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les 35; Conserv
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178..183
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Pred. No. 1.7e-16;
9; Mismatches 11;
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NY
XX
XX
Alpha-helical protein zsig83, its antibodies and the polynucleotide
PT encoding the protein useful for treating disorders associated with
PT abnormal cell growth e.g. cancer and agonists useful for treating
PT wounds
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XX
Claim 1; Page 73-74; 83pp; English.

CC
CT this invention relates to a novel human alpha-helical protein designated
CC zsig83, Zsig83 plays a role in the process of cell growth,
CC differentiation, or proliferation. The zsig83 gene is located on
CC chromosome 22 at position 22q13.1-q13.2. Included in the invention are
CC containing the zsig83 DNA sequence, a cultured cell containing the
CC expression vector, and antibodies specific to the zsig83 protein. The
CC sig83 protein contains 5 alpha helix regions (represented by sequences
CC AAY94677-Y94681) and also contains epitope bearing regions (represented
CC by sequences AAY94688-Y94698) to which the antibodies are directed. The
CC conditions and metastasis and antibodies are used for treating disorders
CC associated with abnormal cell growth e.g. cancer, degenerative
CC conditions and metastasis. The zsig83 protein and its agonists or
CC conditions and metastasis. The zsig83 protein and its agonists or
CC conditions a diagnostic indicator of cancer.
CC the used as a diagnostic indicator of cancer.
CC The present sequence represents the human zsig83 protein.
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ş Ş Search completed: October 11, 2002, 02:42:03 Job time : 32 secs В 밁 Query Match 25.8 Best Local Similarity 36.0 Matches 40; Conservative 15 29 RGTMDGRVQL---MKALLAGPLRPAARRWRNPIPFPETFDGDTDRLPEFIVQTCSYMFVD 85 25.8%; Score 197; DB 21; 36.0%; Pred. No. 1.9e-15; tive 25; Mismatches 40 40; Length 184; Indels 6; Gaps 2

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OM protein -
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R;Anaya, N.; Roncero, M.I.G.
Mol. Gen. Genet. 249, 637-647, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gag polyprotein homolog - fungus (Fusarium oxysporum) retrotransposon skippy
C;Species: Fusarium oxysporum
C;Date: 15-Feb_1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
S60178
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A;Title: Skippy, a retrotransposon from the fungal plant pathogen Fusarium oxyspo
A;Reference number: S60178, MUID:96132549
A;Accession: S60178
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                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-853 <ANA>
A;Cross-references: EMBL:L34658; NID:g510695;
                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: retrotransposon skippy
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PIDN:AAA88790.1; PID:g510696

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66	66	66	66	66	66	66.5	66.5	66.5	66.5	66.5	66.5	66.5	66.5	66.5	66.5
8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7
1498	1058	875	290	290	130	1140	1140	914	914	769	441	430	337	325	269
ν	N	N	N	N	N	N	N	_	<u>س</u>	2	N	2	2	N	N
S53577	T19282	F70755	S69841	S41555	F95328	T20984	F88349	S07047	JN0550	н97033	A96759	F87112	A53041	G72020	G90261
,	hypothetical prote		٠.	TyA protein - yeas	hypothetical prote	hypothetical prote	protein F15D4.7 [i	iodide peroxidase	iodide peroxidase	alpha-glucosidase	protein serine car	SRP	effector cell prot	3′(2′),5′-bisphosp	serine/threonine p

ALIGNMENTS

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R; Farman, M.L.; Tosa, Y.; Nitta, N.; Leong, S.A. Wol. Gen. Genet. 251, 665-674, 1996
A; Title: MAGGY, a retrotransposon in the genome of A; Reference number: Z18882; MUID:96335141
A; Accession: T18347
                                                                                                                                                                                                                                                                                            gag protein homolog, truncated - rice blast fungus magnaporthe gypsy retrotranspc
C;Species: Magnaporthe grisea (rice blast fungus)
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C;Accession: T18347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Mobile element: retrotransposon skippy C;Keywords: polyprotein
                                                                                                   A; Molecule type: DNA
A; Residues: 1-457 <FAR>
A; Cross-references: EMBL:L35053; NID:g522300; PID:g522301; PIDN:AAA33419.1
                                         A; Mobile element:
                                                           A;Gene: gag
                                                                                 C; Genetics:
                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
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Query Match
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Score 104; DB 2;
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hes 31;
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Length 457;
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92

DALKVTFLITRLTG---PALQWVIPYIRKESPL--LNDYRGFLAEMKRVFGWEED

141

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A; Molecule type: DNA
A; Residues: 1-639 <MCH>
A; Residues: 1-639 <MCH>
A; Cross-references: EMBL: Z11866; NID: g2562; PIDN: CAA77890.1; PID: g2563
A; Note: the authors translated the codon ACC for residue 55 as Ala, CAA
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
S23569
                                                                                                                                                                                                                                                                                                        C;Accession: JC6323
R;Anton, B.P.; Helter, D.F.; Benner, J.S.; Hess, E.J.; Greenough, L.; Moran, L.S.; Gene 187, 19-27, 1997
A;Title: Cloning and characterization of the BglII restriction-modification system A;Reference number: JC6322; MUID:97225792
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
JC6323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Mobile element: retrotransposon CfT-1 C; Superfamily: Cladosporium fulvum prob C; Keywords: polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;McHale, M.T.; Roberts, I.N.; Noble, S.M.; Beaumont, Mol. Gen. Genet. 233, 337-347, 1992
A;Title: CfT-I: an LTR-retrotransposon in Cladosporium A;Reference number: S23569; MUID:92318885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gag polyprotein homolog - fungus (Cladosporium fulvum) retrotrar
C;Species: Cladosporium fulvum
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change
C;Accession: S23569; S19849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                                                                endonuclease (EC 3.1.21.-) - Bacillus globigii
C;Species: Bacillus globigii
C;Date: 14-May-1998 #sequence_revision 29-May-1998 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
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                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-23 <ANT>
A; Residues: 1-23 <ANT>
A; Cross-references: GB:U49842;
A; Experimental source: RUB562
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                                                                                                                                                                                A;Gene:
                                                                                                                                                                                                   C; Genetics
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Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                             Superfamily: Bacillus globigii endonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49
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 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PETFDGDTDRLPEFIVQTCSYMEVDENTFSNDALKVTFLITRLTGPALQWVIPYIRK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLILPKMVGGTPQFGDYTDLLQYLEEAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QWVIPYIRKESPLLNDYRGFLAEMKRVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAARRWRNP I PEPETEDGDTDRLPEF I VOTCSYMEVDENTESNDALKVTFLITRLTGPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PASARLSERLPDPDKFTGARSDLRRFATQIRGKMTSNKDRFPNPESRLIYIAGRLSGKAY 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNGEDNADGVFKSYNHLKHAMKSVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEFFYGDRVKFDTWVSQMDMYFLFNSMT----ENLKPIFATTFLRGRAQHWVKPFLRKYLD
 KHWKNNIPIPKRFDFLGTDIDFGKRDTLVE--VQFSNYPFLLNNTVRSELFHKSNMDIDE 121
                                      RRWRNPIPFPETFD-----
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                                                                                                                                              hydrolase
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                                                                                         Similarity
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                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.1%;
30.2%;
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                                                                                       10.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fulvum probable gag
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                                                                          16;
                                      -GDTDRLPEFIVQTCSYMFVDENT------
                                                                      Score 78; DB Pred. No. 0.97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8;
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Pred. No.
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7; Mismatches
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0.63;
                                                                                                          DB 2;
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                                                                          36;
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                                                                                                          Length 223
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β 8

PEKFDGNPDMLGPFMYQCQLFMEKSTRDFSVDRIRVCFVTSMLIGRA

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C; Species: Caulobacter crescentus C; Date: 20-Apr-2001 #sequence_revision C; Accession: E87416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelber; B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; In, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999
C;Accession: JE0163
R;Steplewski, A.; Krynska, B.; Tretiakova, A.; Haas, S.; Khalili, K.; Amini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
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                                                                                                                     A;Experimental source: brain C;Keywords: phosphotroitein C;Keywords: phosphotroitein F;40-60/Domain: transmembrane #status predicted <TMM> F;31,175/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status F;31,142,185,201/Binding site: phosphate (Ser) (covalent) (by casein kinase II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  myelin expression factor-3 - mouse
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A;Accession: E87416
                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-232 <STE>
                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: JE0163
                                                                                                                                                                                                                                                                                                           A; Title: MyEF-3, a
                                                                                                                                                                                                                                                                                                                                                                                                                               N; Alternate names: MyEF-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type:
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Best I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 RRKYLFDOHEFTRRAIEESDTV--KAELLEGVKMFLGEDFDVAKHFTPRYRPWRQRIAFV 309
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61
                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIDGOPLDFAKTVTYRGMMFTGVPNLVWVFGYFRASWTLRADLIGDFVCRLLAHMEKTGA 427
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PETFDGDTDRLPEFIVQTCSYMFVDENTFSNDALKVTFLITRLTGPA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
46; Conserv
                                          18;
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                                          Conservative
                                                                                                                                                                                                                                                                                                           Res. Commun. 243, 295-301, 1 developmentally controlled
                                                                                                                                                                                                                                                                                                                                                Krynska, B.; Tretiakova, A.; Haas, S.; Khalili, K.; Amini,
                                                                                                                                                                                                                                                                                        JE0163;
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                                                              10.1%;
38.3%;
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                                                                                                                                                                                                                                                                                          MUID: 98139908
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1; Mismatches
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                                                              Score 77; DB
Pred. No. 1.3;
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                                          Mismatches
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                                                                                                                                                                                                                                                                                                                brain-derived
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                                                                                   Length 232;
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R;Llaca, V.; Messing, J.
submitted to the EMBL Data Library, October 1997
A;Description: Structure and organization of the 22-kDa
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C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999
C;Accession: T01324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.;
A;Title: Declphering the biology of Mycobacterium A;Reference number: A70500; MUID:98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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A; Residues: 1-464 <LLA>
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RESULT 9
G83758
oligoendopeptidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: F70778
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                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                        ;Cross-references: GB:Z70692; GB:AL123456; NID:g3261567;
;Experimental source: strain H37Rv
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                                                                                             ATVLVGTPAPGPNGSNSDGDSERASQDVRDTAA 233
                                                                                                                                                                          ::: | |:
LKYSRDLAFTAATAYADAAEARGTWDSRMEASWVDAVVRGDTGPELLSRAAALNWDTTAP 200
                                                                                                                                                                                                               MRFRRRLSADPHATQRNSAEARGTMDGRVQ--LMKALLAGPLRP-----AARRW-----
                                                                                                                                  ----RNPIPFP--ETFDGDTDRLPEFIVQTCS 80
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    BH0871 [imported] -
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                                                                                                                                                                                                                                                                            9.7%;
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    Bacillus halodurans (strain C-125)
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                                                                                                                                                                                                                                                                                              Length 414;
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RESULT T35628

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Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodura A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Gerescon: G83758
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C;Date: 01-Dec-2000 #sequence_revision
C;Accession: G83758
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A; Residues: 1-589 <STO>
                                                                                                                                                                                                                                                                                                        C;Function:
A;Description: hydrolyzes alpha-1,6 and alpha-1,4 linkages in starch-related pol:
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: Z16389; MUID:97438521
A; Accession: T08162
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A; Title: Cloning, sequencing, and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Dong, G.; Vieille, C.; Zeikus, J.G.
Appl. Environ. Microbiol. 63, 3577-3584, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Pyrococcus furiosus C; Date: 21-May-1999 #sequence_1
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A; Residues: 1-853 < DON>
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Best Local Similarity 22.7%;
                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
                                                                              199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 KKETPLFASTLNHLAGFRLNLYRARGWND
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258
                                     104 --- TGPALQWVIPYIRKESPLLNDYRGFLAEMKRVFGWEEDED 143
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                                                                                                                                                                                               21 TQRNSAEARGTMDGRVQLMKALLAGPLRPAARRWRNPIPFPETFDGDTDRLPE-----
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                                                                                                                                                      TDENGNPIRDFWDRYTELKDKMLA-----AKQKYAN-LPLEEQKVAVTNEFTEQDYIDLA 198
                                                                            VLFNLAWIDYNYIISTPELKALYDKVDEGGYTREDLK-TVLYHQMWLLNNTFKEHEKINL
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Pred. No. 9
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Pred. No. 17;
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    FGWSEDFD 289
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K; Seeger, K.J.; Harris, D.;
submitted to the EMBL Data L
A; Reference number: Z21584
A; Accession: T35628
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C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_chan
C;Accession: T35628
                                                                                                                                                                                                                                                                                                                                                                                                     Submitted to the EMBL Data Library, September 1995
A;Reference number: Z19389
A;Accession: T21194
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-550 <WIL>
A;Residues: 1-550 <WIL>
A;Cross-references: EMBL:Z54271; PIDN:CAA91032.1; GSPDB:GN00022; CESP:F21D5.1
A;Experimental source: clone F21D5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F21D5.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000 C;Accession: T21194
R;BerKs, M.
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A;Map position: 4
A;Introns: 33/1; 97/3; 213/2; 329/3; 409/2; 512/2
C;Superfamily: Caenorhabditis elegans hypothetical protein F2ID5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 RTKLTNEADGCRNASLREAFEWSCNTVFAKLGVDVGVRGWTAMAEAFGFNDDGLRVPFPV
327
                                        118 ESPLLNDY 125
                                                                                284 SFDGDADRLMYFRAK
                                                                                                                                                               230 RFRNLLERIPSSLLEVEFRNESEELNQGCGADFVKISQKLPAN-FSPTAAE-----PKCA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 RRLSADPHATQRNSAEAR----GTMDGRVQLMKALLAGPLRPAARRWRNPIPFPETFDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                       63 TFDGDTDRLPEFIVQTCSYMFVDENTFSNDAL-----KVTFLITRLTGPALQWVIPYIRK 117
                                                                                                                                                                                                     9 RFRRRLSADPHATQ----RNSAEA--RGTMDGRVQLMKALLAGPLRPAARRWRNPIPFPE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDRLP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRLNADPDKPMLNRAVSRTYPPGSTFKVYTAAAALEAGVIRDLDAPTRSPDPY--TLPGT
Q---LKDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                 9.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; James, K.D.; Parkhill, J.; Barrell, Library, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFIVOTCSYMF----VDENT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 71.5;
Pred. No. 1
                                                                                                                                                                                                                                                                 Score 71.5;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSPDB:GN00070; SCOEDB:SC6G9.32
                                                                                                                                                                                                                                                                                  Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----FSNDALKVTFLI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B.G.; Rajandream,
                                                                                  VTYIRE 326
                                                                                                                                                                                                                                                37;
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250
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D82550

RESULT 13

Query Match 9.2%; Best Local Similarity 22.7%; Matches 22; Conservative

18;

Score 70.5; Pred. No. 14; Mismatches

DB

2; 32;

Length Indels

443;

25;

Gaps

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A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajina, J.P.; Krieger, J.E.; Kuramae, E.B.; chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Marti A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri Rodriques, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Se A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, Tsphako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein XF2493 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
S59771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: D82550
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide S
                                                                                                                                                                                                                                                                                                                                                    hypothetical protein YPR106w - yeast (Saccharomyces N;Alternate names: hypothetical protein P8283.9 N;Alternate names: cerevisiae C;Species: Saccharomyces cerevisiae C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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A; Residues: 1-180 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: XF2493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE004057; GB:AE003849; NID:g9107690; PIDN:AAF85291.1; GSPDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: D82550
A; Map
                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-443 <NEL>
                                                                                                                                                                                        A; Reference number: A; Accession: S59771
                                                                                                                                                                                                                                           submitted to the EMBL Data Library, July 1995 A; Description: The sequence of S. cerevisiae
                                                                                                                                                                                                                                                                                                   R; Nelson
                                                                                                                                                                                                                                                                                                                          C; Accession: S59771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A59328
                         A; Cross-references:
                                                                                                        A;Cross-references: EMBL:U32445; NID:g914969; PID:g914977; MIPS:YPR106w
                                                                            ; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 SFQ 172
position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 ALQ 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 PAL-LRFQARLVLGHRDPTTHLQARLAAAALGTW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 PTLDMRFRRRL---SADP--HATQRNSAEARGTMDGRVQLMKALLAGPLRPAARRWRNPI
                                                   SGD: ISR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTDPCRVIAIYPDEFNAELDRYVVWTVEWQQPVFLGNSAWTHAGTLPTHLWLSFTPQTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-----FPETFDGDTDRLPEFIVQTCSYMFVDENTFSNDALKVTFL---ITRLTGP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa hypothetical protein PRF10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                       S59764
                                                                                                                                                                                                                                                                                                                                                      *sequence_revision 01-Mar-1996 *text_change 06-Feb-1998
                            SGD:S0006310; MIPS:YPR106w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.2%; Score 70.5; D
26.8%; Pred. No. 4.7;
tive 16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
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T42607
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C;Species: equine herpesvirus 4
A;Variety: strain NS80567
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T42607; T42622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Holecule type: DNA
A;Residues: 1-1442 <TE2>
A;Cross-references: EMBL:AF030027; NID:g2605950; PIDN:AAC59599.1; PID:g2606027
A;Experimental source: strain NS80567
Search completed: October 11, 2002, 02:43:41
Job time: 23 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
J. Gen. Virol. 79, 1197-1203, 1998
N;Title: The DNA sequence of equine herpesvirus-4.
N;Reference number: Z22173; MUID:98264497
N;Accession: T42607
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.2%; Score 70; DB 2; Length 1442; Best Local Similarity 23.6%; Pred. No. 70; Matches 33; Conservative 15; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary; translated from GB/EMBL/DDBJ
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Cross-references: EMBL:AF030027; NID:g2605950; PIDN:AAC59599.1; PID:g2606027
Experimental source: strain NS80567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccession: T42622
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                                                                                                   1073 REPLWSDIKGGLSALLAALG 1092
                                                                                                                                                                                                    1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 SQWLINALLKKDPINLNMLRNDLFQDWKSELALLSRI 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 PELIDSSSDHVPTFESDLYAVGLCLLSFISQHEPYNE---LQALVSHGSSPGIGSSSIQQ 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 -QWVIPYIRKESP-----LINDYRGFLAEMKRV 135
                                                                                                                                              118 ESPLINDYRGFLAEMKRVFG 137
                                                                                                                                                                                                                                                                                                  985 PLFPEAMRPALTFDPQALATIAARCNGPPAREG-ARFGELAASGPLRRRA-AMMNQIPDP 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 ETFDGDTDRLPEFIVQTCSYMFVDENTFSNDALKVTFLITRLTGPALQWVIPYIR----K 117
                                                                                                                                                                                                                                                                                                                                              4 PTLDMRFRRRLSADPHATQRNSAEARG--TMDGRVQLMKALLAGPLRPAARRWRNPIPFP 61
                                                                                                                                                                                                         -VKVVVLYSPLPDEDLLGGLPTTRPGGSR 1072
                                                                                                                                                                                                                                                                                                                                                                                                        38;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                         Score
seq length: 0
seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    October 11, 2002, 02:39:39 ; Search time 11 Seconds (without alignments) 506.874 Million cell updates/sec
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
                  Length
488
875
989
2009
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822
4822
4822
369
369
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1487
906
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914
914
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                                                                                                                                                            SYK_MYCFE
YC78_MYCTU
RPOC_LEUME
SEC7_YEAST
                                                                                                                                                                                                                              CYPK_STRCO
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OASL_HUMAN
                                                                                                                                                                                                                                                                                    YM42_MYCTU
NAC1_MOUSE
                         ICP4_HSVEB
FOX2_CANTR
IMB2_SCHPO
DYHC_DROME
FMR1_MOUSE
LON_CHLTR
RLR1_YEAST
IF5_SCHPO
G3PA_GRAVE
                                                                                            AMPN_CAUCR
ATNA_DROME
                                                                                                                       LATX_PAPSO
HIFA_MOUSE
BIR6_HUMAN
HA1K_MOUSE
                                                                                                                                                                                                                    FTSY_MYCLE
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                                                                                                                                                                                                   PERT_RAT
                 CL11_HUMAN
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                                                                                                                                                                                                          Q02055 streptomyce
Q01728 rattus norv
Q33010 mycobacteri
P35419 mus musculu
                                                       014089
P37276
                                                                          P28925
P22414
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Q61221
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P11075
                                                                                                                                                                                                                                                         P39109
Q09689
P30724
                            P35922 mus musculu
084348 chlamydia t
P53552 saccharomyc
                                                                                                                                                                               P14650 rattus norv
Q49158 mycoplasma
Q11042 mycobacteri
                                                                                                                                                                                                                                                 Q15646
                                                                                                                                                                                                                                                                                               Q10523
                                                                                                                                                                                                                                                                                                                          Description
                  P20809
                                                                                                              9 homo sapien
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ID LDO1_HUMAN
STANDARD; PRT; 146 AA.
ID C 095751;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE LDOC1 protein (Leucine zipper protein down-regulated in the LDOC1.
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ALIGNMENTS

Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

cancer cells).

NCBI_TaxID=9606;

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NAC1_MOUSE
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Q10523;
01-OCT-1996
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Hypothetical 44.6 kDa protein Rv2242.
RV2242 OR MT2302 OR MTCY427.23.
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Tuberculist; Rv2242; .
Hypothetical protein; Complete proteome.
Protein; Complete proteome.
Promise 414 AA; 44637 MW; F454D43397711F73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
-i- SIMILARITY: BELONGS TO THE CDAR FAMILY.
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01-NOV-1997 (Rel. 3
01-MAR-2002 (Rel. 4
Sodium/calcium excl
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Ann. N.Y. Acad. Sci. 779:126-128(1996).
IN Y. Acad. Sci. 779:126-128(1996).
COUPLING. RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION
COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION
SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
SO ENZYME REGULATION: BY ATP...
SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
TISSUE SPECIFICITY: CARDIAC SARCOLEMMA.
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InterPro; IPR003644; Calx_beta.
InterPro; IPR002613; Na_Ca_Ex.
Pfam; PF01699; Na_Ca_Ex; 2.
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"Cloning of the mouse cardiac Na(+)-Ca2+ exchanger
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MEDLINE-96250070;
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Mammalia; Eutheria;
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el. 41, Last annotation update)
exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
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  Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88067705; PubMed-2891103;
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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pfam; pF00297; Ribosomal_L3; 1.
proDom; pP001374; Ribosomal_L3; 1.
pROSITE; pS00474; RIBOSOMAL_L3; 1.
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01-NOV-1988 (Rel. 09, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
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01-NOV-1988
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-I- SIMILARITY:
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                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BELONGS TO THE L3P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: Mitochondrial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.7%;
27.0%;
                                                                                                                                                                                                      Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    692
760
389
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157
866
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                                                                                                                                                                                 38632 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  rmatics Institute. There are no resi
                                                                                                             9.0%;
29.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                             Score 69;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 74; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (PO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-ASP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                    6DE6B5BD6BD72E32, CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
                                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage by
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                                                                                                                                  Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration -
                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                    for
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                                                                                        Gaps
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REAL DESCRIPTION OF THE PROPERTY OF THE PROPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ICP4_HSVEK P17473;
                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P04002; 1WFA.
HSSP; P04002; 1WFA.
Early protein; Transcription regulation; Trans-acting DNA-binding; Phosphorylation; Nuclear protein.
DNA-DINGHOUSE PROTECTION OF TWO PARTICH.
DOMAIN 181 213 STOTE PARTICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harty R.N., Colle C.F. III, Grundy F.J., O'Callaghan D.J.;
"Mapping the termini and intron of the spliced immediate-early
transcript of equine herpesvirus 1.";
J. Virol. 63:5101-5110(1999).
-i- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE
OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING
OTHER VIRAL GENES, AND AUTOREGULATING TO DNA, SYNTHESIS.
-i- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
-i- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=89370304; PubMed=2549711;

Raumann R.P., O'Callaghan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Equine herpesvirus type 1 (strain Kentucky A) (EHV-1).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel.
01-AUG-1990 (Rel.
01-FEB-1994 (Rel.
                                                           1089
                                                                                                                                                                         1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J04366; AAA46089.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-90064773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "DNA sequence and comparative analyses of the 1 immediate early gene."; virology 172:223-236(1989).
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M30498; AAA66554.1; PIR; A33764; EDBEE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IE OR 64.
                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
124 DYRGFLAEMKRVFG
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                                                                                                                                                                            WRPALTFDPQALATIAARCSGPPARDG-ARLGELAASGPLRRRA-AWMHQIPDPED----
                                                                                                                                                                                                                                 FRRRLSADPHATQRNSAEARG--TMDGRVQLMKALLAGPLRPAARRWRNPIPFPETFDGD
                                                                                                                TDRLPEFIVQTCSYMFVDENTFSNDALKVTFLITRLTGPALQWVIPYIR----KESPLLN
                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-profit institutions as long as and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF 1432-1487 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        1487 AA;
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcriptional protein ICP4 (155
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15, Last sequence update)
28, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=2555546;
                                                                                                                                                                                                                                                                                                                                                                                                                                      931
                                                                                                                                                                                                                                                                                                                     24.6%;
                                                                                                                                                                                                                                                                                                                                                                                                        154716 MW; 044E39A570608A6B CRC64;
                                                                                                                                                                                                                                                                                                                                               9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                                                                                               Score 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ARG/LYS-RICH (BASIC)
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                                                              VKVVVLYSPLQDEDLLGGLPASRPGGSRREPLWS
                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                  Length 1487;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor;
                                                                                                                                                                                                                                                                                             38;
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RESULT 6
YCFI_YEAST

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EMBL; L35237; i
EMBL; Z48179; (
HSSP; P13569; 1
SGD; S0002542;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20253522; PubMed=10790694; Petrovic S., Pascolo L., Gallo R., Cupelli F., Ostrow J.D., Goffeau A., Tiribelli C., Bruschi C.V.; "The products of YCF1 and YLL015w (BPT1) cooperate for the dependent vacuolar transport of unconjugated bilirubin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-S288C / AB972;
Oliver K., Harris D., Barrell B.G., Rajandream M.A.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Szczypka M.S., Wemmie J.A., Moye-Rowley S.W., Thiele D.J.; "A yeast metal resistance protein similar to human cystic fibrosis transmembrane conductance regulator (CFTR) and multidrug resistance
            TRANSMEN
                         TRANSMEM DOMAIN
                                                     TRANSMEM
DOMAIN
                                                                                                                                                                                           InterPro; IPR003593; Awa.
InterPro; IPR001140; ABC_transporter_tmem
InterPro; IPR003439; ABC_transportr.
InterPro; IPR003439; ABC_membrane; 2.
                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb
                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae.";
Yeast 16:561-571(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             associated protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                      SMART; SM00382; AAA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ÷
                                                                                                                                                                                  Pfam; PF00064; ABC_membrane; Pfam; PF00005; ABC_tran; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷
                                                                                                TRANSMEM
                                                                                                                DOMAIN
                                                                                                                                         ATP-binding;
                                                                                                                                                         PROSITE;
                                                                                                                            Cadmium resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: COOPERATES FOR THE ATP-DEPENDENT VACUOLAR TRANSPORT OF
                                                                                                                                                                                                                                                            S0002542; YCF1.
PS00211; ABC_TRANSPORTER;
ing; Transmembrane; Glycop
                                                                                                                                                                                                                                                                         1NBD
                                                                                                                                                                                                                                                                                      AAA50353.1;
CAA88217.1;
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         1 (BY SIMILARITY).

1 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

2 (BY SIMILARITY).

EXTRACELLULAR (BY SIMILARITY).

3 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

4 (BY SIMILARITY).
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UENCE LINE=9 tmann 90ASL,	Homo sapiens (Human Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;	015646; 075686; 09Y6K7; 09Y0F 01-NOV-1997 (Rel. 35, Created 30-MAY-2000 (Rel. 39, Last se 16-OCT-2001 (Rel. 40, Last ar 59 kDa 2'-5'-oligoadenylate s (p590ASL) (Thyroid receptor i	141 DEDF : 1148 QKRF 1148 QKRF JLT 7 L_HUMAN OASL_HUMAN	106 PALQW- : 1088 TTWQFI	55 RNPIPFPET : 1035 RAPMTFFET	Query Match Best Local S: Matches 29;	CONFLICT	MUTAGEN	NP_BIND	DOMAIN NP_BIND	TRANSMEM	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN TRANSMEM	DOMAIN	DOMAIN	DOMAIN
134; 1se -5'	ens (Human); Metazoa; Eutheria; D=9606;	75686; Q 97 (Rel. 00 (Rel. 01 (Rel. -5'-olig	144 1151 N ST	WVIP- : : FIFIIIPL	TPI	h Similarity 29; Conser		713 908	1306	1227	1202	1110	1088	1024	965	594	552	468	444	367 423	300	191	152 170
PubMed=9722630; pubMed=9722630; n H.S., Widder S oligoadenylate d to the 2'-5' o	an). a; Chordata a; Primates	9Y6K7; Q9Y6K6 35, Created) 39, Last seq 40, Last anno oadenylate syn d receptor in	TANDARD;	SVFYIYYQQYY	RILNR	9.0%; 23.4%; vative	680 AA; 171120	713 908	863 1313	1515								530	446	422	345	278	169 190
2263); dder S., Joergensen R., Justesen J.; dder S., Joergensen III, ylate synthetase like protein: a novel ylate synthetase family.";	a; Craniata; Vertebrata; Euteleostomi; s; Catarrhini; Hominidae; Homo.	yY6K6; ited) : sequence update) : annotation update) :e synthetase like protein (p59 OASL) or interacting protein 14) (TRIP14).	ζ.	PALQWVIPYIR	FDGDTDRLPEFIVQTCSYMFVDENTFSNDALKVTFLITRLTG 105	Score 68.5; DB 1; Length 1515; Pred. No. 30; 19; Mismatches 35; Indels 41; Gaps	R (IN REF 0F92FDDBA	MISSING: LOSS OF FUNCTION. S->A: LOSS OF FUNCTION.	(BV CARK)	CYTOPLASMIC (BY SIMILARITY). ATP (POTENTIAL).	EXTRACELULAR (BY SIMILARITY). 17 (BY SIMILARITY).	CYTOPLASMIC (BY SIMILARITY). 15 (BY STWILARITY)	14 (BY SIMILARITY). EXTRACELLULAR (BY SIMILARITY). 15 (BY SIMILARITY).	CYTOPLASMIC (BY SIMILARITY).	EXTRACELLULAR (BY SIMILARITY).	CYTOPLASMIC (BY SIMILARITY).	EXTRACELLULAR (BY SIMILARITY).	CYTOPLASMIC (BY SIMILARITY).		CYTOPLASMIC (BY SIMILARITY). 8 (BY SIMILARITY).	EXTRACELLULAR (BY SIMILARITY). 7 (BY SIMILARITY)	YY S	EXTRACELLULAR (BY SIMILARITY). 5 (BY SIMILARITY)

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                                                                                                                                                                                                                                                                                                                                                        EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore D.D.; "Two classes of proteins dependent on either the presence or absence of thyroid hormone for interaction with the thyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rebouillat D., Marie I., Hovanessian A.G.;
"Molecular cloning and characterization of two related and interferon-
induced 56-kDa and 30-kDa proteins highly similar to 2'-5'
oligoadenylate synthetase.";
                              VARSPLIC CONFLICT
                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                         InterPro; IPR001797; 25A_synth.
InterPro; IPR001201; PAP_25A_core
InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 2.
SMART; SM00213; UBQ; 2.
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CONFLICT
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                                                                                                VARSPLIC
                                                                                                               NIAMOC
                                                                                                                                             RNA-binding;
                                                                                                                                                            PROSITE;
                                                                                                                                                                                                            PROSITE; PS00832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDED RNA AND DAA:
SUBUNIT: SPECIFICALLY INTERACTS WITH THE LIGAND BINDING DOMAIN OF
THE THYROID RECEPTOR (TR). TRIP14 DOES NOT REQUIRE THE PRESENCE OF
THYROID HORMONE FOR ITS INTERACTION.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; P56 (SHOWN HERE) AND P30; MAY BE
PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES, WITH THE HIGHEST
LEVELS IN PRIMARY BLOOD LEUKOCYTES AND OTHER HEMATOPOIETIC SYSTEM
TISSUES, COLON, STOMACH AND TO SOME EXTENT IN TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAUTION: THIS MAY NOT BE THE TRUE ORTHOLOG OF MOUSE OASL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDUCTION: BY INTERFERONS.

SIMILARITY: BELONGS TO THE 2-5A SYNTHETASE FAMILY.

SIMILARITY: CONTAINS 2 UBIQUITIN-LIKE DOMAINS.

CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS
TO 416 DUE TO A FRAMESHIFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: DOES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endocrinol. 9:243-254(1995).
UNCTION: DOES NOT HAVE 2'-5'-0AS ACTIVITY, BUT BINDS DOUBLE-
                                                                                                                                                                                                                                                                                                                        AF063611; AAD28541.1; -.
AF063612; AAD28542.1; -.
293097; -; NOT_ANNOTATED_CDS.
L40387; AAC41733.1; ALT_FRAME
P02248; 1UBI.
                                                                                                                                                                                                                                                                                                                                                                                                         AJ225089; CAA12396.1; -.
                                                                                                                                                         PS00832; 25A_SYNTH_1; 1.
PS00833; 25A_SYNTH_2; 1.
PS50152; 25A_SYNTH_3; 1.
PS50053; UBIQUITIN_2; 1.
                            256
26
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89
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38
89
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                                                                          ITIN_2; 1.

induction; Alternative splicing; Repeat. . . .

BIQUITIN-LIKE 1.

BIQUITIN-LIKE 2.

YVKARSPRANLPPLYALELLTIYAWEMGTEEDENFM ->

YVKARSPRANLPPLYALELLTIYAWEMGTEEDENFM ->
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Best Local
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CONFLICT
                                                             This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                     Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases -:- FUNCTION: IS NEEDED FOR CORRECT CYCLIZATION OF THE LEADING TO ISOCHROMANEQUINONE FORMATION.
                                                                                                                                                                                                                                                                                                  genes of Streptomyces coelicolor A3(2) including the polyketide synthase for the antibiotic actinorhodin.";
J. Biol. Chem. 267:19278-19290(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Actinorhodin polyketide synthase bifunctional
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         EMBL; X63449; CAA45046.1;
EMBL; AL593842; CAC44203.1
PIR; S25843; S25843.
                                                                                                                                                                                                                               Rajandream M.A.;
                                                                                                                                                                                                                                                        STRAIN=A3(2);
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence and deduced functions of a set of cotranscribed
                                                                                                                                                                                                                                                                                                                                                      Malpartida F.
                                                                                                                                                                                                                                                                                                                                                                   Fernandez-Moreno M.A., Martinez E.,
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=A3(2) / M145;
MEDLINE=92406871; PubMed=1527048;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCBAC28G1.16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q02055;
                                                                                                                                                                                                                                             Warren T., Harris D., Cerdeno A.M., Parkhill J.,
                                                                                                                                                                         -!- PATHWAY: BIOSYNTHESIS OF POLYKETIDE ANTIBIOTIC ACTINORHODIN.
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                        CAC44203.1;
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A -> S (IN REF. 2).
Y -> I (IN REF. 2).
I -> T (IN REF. 2).
O -> L (IN REF. 2).
NP -> KG (IN REF. 4).
S -> T (IN REF. 2; AAD28541).
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Query Match
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Q01728;
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01-JUN-1994 (Rel.
01-MAR-2002 (Rel.
                                                                                                             "Cloning of a third mammalian Na+-Ca2+ exchanger, J. Biol. Chem. 271:24914-24921(1996).
-!- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCIP
                                                                                                                                                                                                                                       MEDLINE-94253030; pubMed-8195112;
Lee S.-L., Yu A.S.L., Lytton J.;
"Tissue-specific expression of Na(+)-Ca2+ exchanger isoforms.";
J. Biol. Chem. 269:14849-14852(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93138118; PubMed-8422940;
Low W., Kasir J., Rahamimoff H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JNAR-2002 (Rel. 41, Last annotation update)
Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
                                                                                                                                                                                TISSUE SPECIFICITY.
STRAIN-SPRAGUE-DAWLEY;
MEDLINE-96394663; PubMed-8798769;
                                                                                                                                                                                                                                                                                                                                           FEBS
                                                                                                                                                                                                                                                                                                                                                                   *Cloning of two isoforms of the rat brain Na(+)-Ca2+ exchanger gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING STRAIN-SPRAGUE-DAWLEY; TISSUE-Kidney cortex;
                                                                                                                                                        Philipson K.D.;
                                                                                                                                                                  Nicoll D.A., Quednau B.D., Qui Z.,
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93202244; PubMed=8454039;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                          their functional expression in HeLa cells. S Lett. 319:105-109(1993).
                       FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION
COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION
SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
ENZYME REGULATION: BY ATP.
SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane
ALTERNATIVE PRODUCTS: 5 isoforms; heart/NACA1 (shown here),
brain 1/NACA5, brain 2/NACA4, kidney 1/NACA7 and kidney 2/NACA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLRVTFRQELTQPPIASMGGSWEFRGDGDGTEVVLTHDFAAVDEAALPG-LREALDANSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ning of the rat heart Na(+)-Ca2+ ession in HeLa cells.";
Lett. 316:63-67(1993).
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produced by alternative splicing.
SUE SPECIFICITY: CARDIAC SARCOLEMMA OR BRAIN,
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29.0%;
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Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                     Rahamimoff H.;
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AND SPLEEN
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                            2/NACA3;
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 EMBL; X68191; CAA48273.1;
EMBL; X68812; CAA48707.1;
EMBL; X68813; CAA48708.1;
EMBL; U04933; AAB39952.1;
EMBL; U04934; AAA19124.1;
EMBL; U04936; AAA19125.1;
FIR; S25552; S25552
PIR; S28833; S28833.
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CONFLICT
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InterPro; IPR002613; Na_Ca_Ex.
Pfam; PF01699; Na_Ca_Ex; 2.
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een the Swiss Institute of Bioinformatics and the EN
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ISOFORM 1 AND KIDNEY ISOFORM 2).
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BETA-1.
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CALMODULIN-BINDING (BY SIMILARITY).
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                                                                                                                                                                                                                                                                         BETA-2
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                            (IN BRAIN ISOFORM 2 AND KIDNEY
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ISOFORM 1 AND
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                 InterPro; IPR003593; AAA.
InterPro; IPR001687; ATP_GTP_A.
InterPro; IPR000897; SRP54.
Pfam; PF00448; SRP54; 1.
Pfam; PF02881; SRP54_N; 1.
ProDom; PD000819; SRP54; 1.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simmon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevene v. Smoon S., Simmonds M., Skelton J., Squares R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell division protein ftsy homolog. FTSY OR MI1628 OR MICB250.02.

Mycobacterium leprae gacteris.
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                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- FUNCTION: FUNCTIONAL HOMOLOG OF SRP RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTSY_MYCLE
                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Squares S., Stevens K., Taylor K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21128732; PubMed=11234002;
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed.
SMART; SM00382;
                                                                                                                                                                                Leproma; ML1628;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Membrane-associated (By similarity).
SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: FUNCTIONAL HOMOLOG OF SRP RECEPTOR. PROBABLY INVOLVED THE RECEPTION AND INSERTION OF A SUBSET OF PROTEINS AT THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEMBRANE (BY SIMILARITY)
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                                                                                                                                                                                                            AL583922; CAC
P10121; 1FTS.
                                                                                                                                                                                                                                                                  297369; CAB10596.1;
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971 AA;
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                                                                                                                                                                                                                                            CAC30579.1;
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108184 MW;
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Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                 Usage by
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NP_BIND 28 245 GTP (BY SIMILARITY)

NP_BIND 320 324 GTP (BY SIMILARITY)

NP_BIND 382 385 GTP (BY SIMILARITY)

SEQUENCE 430 AA; 45354 MW; E9F78589AAB2C598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakayama T., Ohtaki S.; "Nucleotide sequence of the cDNA encoding mouse thyroid peroxidase."; Gene 123:289-290(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Thyroid peroxidase precursor (EC 1.11.1.8) (TPO).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IN THYROGLOBULIN TO YIELD THE THYROID
-I- CATALYTIC ACTIVITY: Iodide + H(2)0(2)
-I- COFACTOR: HEME (PROTOPORPHYRIN IX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERT_MOUSE
P35419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6; T:
MEDLINE=93154601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: THYROID HORMONE BIOSYNTHESIS
-!- SUBCELLULAR LOCATION: Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: IODINATION AND COUPLING OF THE HORMONOGENIC TYROSINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kotani T., Umeki K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                        EMBL; X60703; CAA43114.1; ... PIR; JN0550; JN0550.
                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                entities requires a
                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The serious as longues by non-profit institutions as longues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN
                                                                                                                                                       HSSP; P05164; 1
MGD; MGI:98813;
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                                                                            InterPro;
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                                                                                                                                                                                  P05164; 1CXP
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                                                                       IPR002007;
IPR000152;
IPR000561;
                                                    IPR001881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Thyroid;
1; PubMed-7916704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BELONGS TO THE PEROXIDASE FAMILY. XPO SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                 Anim_peroxidase.
Asx_hydroxyl.
EGF-like.
EGF_Ca.
                                                                                                                                                                                                                                                                                                                license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto I., Takeuchi M., Takechi
Peroxdse_3.
Peroxidase.
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Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HORMONES T(3) AND T(4).
* iodine + 2 H(2)0.
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CARBOHYD
SEQUENCE
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P14650;
Ol-APR-1990 (Rel. 14, Created)
Ol-APR-1990 (Rel. 14, Last seq
16-OCT-2001 (Rel. 40, Last ann
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ACT_SITE
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PROSITE; PS001435; PEROXIDASE_1;
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                       MEDLINE-90045972; PubMed-2813071;
Derwahl M., Seto P., Rapoport B.;
"Complete nucleotide sequence of the FRTL5 rat thyroid cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS;
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                                                                                                         SEQUENCE OF 145-914 FROM N.A.
MEDLINE-90114171; PubMed-2691880;
ISOZAKI O., Kohn L.D., Kozak C.A., Kimura S.;
"Thyroid peroxidase: rat cDNA sequence, chromosomal localization mouse, and regulation of gene expression by comparison to thyroglobulin in rat FRTL-5 cells.";
Mol. Endocrinol. 3:1681-1692(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=90045972;
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                      FUNCTION: IDDINATION AND COUPLING OF THE HORMONOGENIC TYROSINES IN THYROGLOBULIN TO YIELD THE THYROID HORMONES T(3) AND T(4). CAPALYTIC ACTIVITY: Iddide + H(2)O(2) = iddine + 2 H(2)O. COPACTOR: HEME (PROTOPORPHYRIN IX).
    PATHWAY: THYROID HORMONE BIOSYNTHESIS.
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40, Last annotation update)
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roxidase; 1.
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DISTAL HISTIDINE (POTENTIAL).
DISTAL ARGININE (POTENTIAL).
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-:- SIMILARITY: CONTAINS 1 EGF-LIKE
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PROSITE; PS00010;
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Pfam; PF00084; sushi;
PRINTS; PR00457; ANPE
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SMART; SM00179; EGF_CA; 1.
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M31655; AAA42265.1;
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; ASX_HYDROXYL;
; PEROXIDASE_1;
; EGF_2; 1.
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PROSITE; PS00339; AA_TRNA_LIGASE_II_2; 1.

Aminoacy1-trNA synthetase; Protein blosynthesis; Ligase; ATP-binding.
SEQUENCE 488 AA; 56703 MW; 6F42D2B514413202 CRC64;
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InterPro; IPR002309; tRNA-synt_2.
InterPro; IPR002313; tRNA-synt_lys_2.
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Infect. Immun. 64:1800-1809(1996)
-i- CATALYTIC ACTIVITY: ATP + L-1
+ L-lysyl-trnA(Lys).
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"Antigenic topology of the P29 surface lipoprotein of Mycoplasma
fermentans: differential display of epitopes results in
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01-OCT-1996 (Rel. 34, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Hypothetical 93.4 kDa protein Rv1278.
RV1278 OR MT1315 OR MTCY50.04C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00982; TRNASYNTHLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96201595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma fermentans.
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                                                            Actinomycetales; Corynebacterineae; NCBI_TaxID=1773;
                                                                                             Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                            Q11042;
                                                                                                                                                                                                                          YC78_MYCTU
MEDLINE=98295987; PubMed=9634230;
                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                      PFPETFDGDTDRLPEFIVQTCSYMFVDENTFSNDALKVTFLI-TRLTGPALQWV-----
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19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                             STANDARD;
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(EC 6.1.1.6) (Lysine--trna ligase) (Lysrs)
                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
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Pred. No.
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                                                                                Mycobacteriaceae;
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RRC OCC GREET

Leuconostoc

Bacteria; Firmicutes; NCBI_TaxID=1245;

Bacillus/Clostridium group;

Lactobacillaceae;

Leuconostoc mesenteroides

SEQUENCE FROM N.A. STRAIN-NCDO 523; MEDLINE-97016803; PubMed-8863429;

15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (T
beta' chain) (RNA polymerase beta' subunit) (Fragment).

2.7.7.6) (Transcriptase

P94892; RPOC_LEUME

STANDARD;

PRT;

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RPOC_LEUME
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               TubercuList; Rv1278; -. Hypothetical protein; Complete SEQUENCE 875 AA; 93350 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Bolcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laboratory strains."; submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 277137; CAB00904.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bishai W.;
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                                                                                                                                          761 PV-FGPSFEVEVDTDLRIRSRTLDDRTVPYECLSGGAKEQLGILARLAGAAL----
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                                                                      KEDAVPVLIDDALGFTDPERLAKMGEVF
                                                                                                          KESP---LINDYRGF-----LAEMKRVF 136
                                                                                                                                                                          PIPEPETEDGDTDRLPEFIVQTCSYMEVDENTESNDALKVTFLITRLTGPALQWVIPVIR 116
                                                                                                                                                                                                                  RKGKLDAAETEREHAASHHARVGRRARAARLLRSVMARHRDTTRLRYVEPYRAELHRLGR 760
                                                                                                                                                                                                                                                     RRLSADPHATQRNSAEARGTMDGR----VQLMKALLA------GPLRPAARRWRN
                                                                                                                                                                                                                                                                                                                                                                                                                      MT1315;
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                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                        8.7%;
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366C580A3AAC97A2 CRC64;
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Best Local Similarity
Matches 44; Conserv
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SEQUENCE
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InterPro; IPR000722; RNA_pol_A.
Pfam; PF00623; RNA_pol_A; 1.
Transferase; DNA-directed RNA polymerase; Transcription.
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-- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
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                                                                                                                                                    781
                                                                                                                                                                                                                                                                                              732 GYLTRRLVDVAQDVIVRE--FDNDSDR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               612 SQVATVTKQFRRGLITDSERYQRVTEIWTKAKDIIQDKLIESFEPTNPIFMMQDSGARGN 671
                                                                                                                                                                                                                         129 LAEMKRVFGWEEDE 142
                                                                                                                                                                                                                                                                                                                                69 DRLPEFIVOTCSYMFVDENTFSNDALKVTFLITRLTGPALQWVIPYIRKESPLLNDYRGF 128
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SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1 BETA' CHAIN.
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989 AA;
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110185 MW; 395E91BE46F43CDC CRC64;
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